

0420/0590

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## RAW SEQUENCE LISTING

DATE: 06/14/2001

PATENT APPLICATION: US/09/871,388

TIME: 10:25:52

Input Set : N:\Crf3\RULE60\09871388.txt  
 Output Set: N:\CRF3\06142001\I871388.raw

## SEQUENCE LISTING

ENTERED

3 (1) GENERAL INFORMATION:  
 4 (i) APPLICANT: Rubin, Gerald M.  
 5 Pan, Duoia  
 6 Rooke, Jenny  
 7 Yavari, Reza  
 8 Xu, Tian  
 9 (ii) TITLE OF INVENTION: KUZ: A Novel Family of Metalloproteases  
 10 (iii) NUMBER OF SEQUENCES: 10  
 11 (iv) CORRESPONDENCE ADDRESS:  
 12 (A) ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
 13 (B) STREET: 268 BUSH STREET, SUITE 3200  
 14 (C) CITY: SAN FRANCISCO  
 15 (D) STATE: CALIFORNIA  
 16 (E) COUNTRY: USA  
 17 (F) ZIP: 94104  
 18 (v) COMPUTER READABLE FORM:  
 19 (A) MEDIUM TYPE: Floppy disk  
 20 (B) COMPUTER: IBM PC compatible  
 21 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 22 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
 24 (vi) CURRENT APPLICATION DATA:  
 C--> 25 (A) APPLICATION NUMBER: US/09/871,388  
 C--> 26 (B) FILING DATE: 31-May-2001  
 27 (C) CLASSIFICATION:  
 29 (vii) PRIOR APPLICATION DATA:  
 30 (A) APPLICATION NUMBER: 08/937,931  
 31 (B) FILING DATE:  
 33 (viii) ATTORNEY/AGENT INFORMATION:  
 34 (A) NAME: OSMAN, RICHARD A  
 35 (B) REGISTRATION NUMBER: 36,627  
 36 (C) REFERENCE/DOCKET NUMBER: B97-081  
 37 (ix) TELECOMMUNICATION INFORMATION:  
 38 (A) TELEPHONE: (415) 343-4341  
 39 (B) TELEFAX: (415) 343-4342  
 41 (2) INFORMATION FOR SEQ ID NO: 1:  
 42 (i) SEQUENCE CHARACTERISTICS:  
 43 (A) LENGTH: 5630 base pairs  
 44 (B) TYPE: nucleic acid  
 45 (C) STRANDEDNESS: double  
 46 (D) TOPOLOGY: linear  
 47 (ii) MOLECULE TYPE: cDNA  
 48 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 49 GTTTAAAAA AACCACCAAG CGAGTTGGAC GCGTAACTCT TTGTAACGGA TCTCGGAACG 60  
 50 CCGTGGGAGT CGGAAAATCG CTGGACGCGT GTTCGTGCGT TTGCATGTGT GCGTGCGTTC 120  
 51 GTGTGTGTGT GTGTGCTAAT GTGCGAGCGG GTGAGCGAAT AAAAATAAAT ATATATCGTC 180  
 52 AAGTCAGGCT TAAGAAATGT GCGCTAATCA AAGAAAATGC CCCCAATTCT GGCCAATTGA 240

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53	GAATTGTGGC	TAAACAAAAA	ATTCGACCGG	AGTTCAAAAA	TAAACAATCC	AGTGAATAAA	300
54	CACACAAAAT	CAATCAAAAA	AGAAGATTTT	TCTTTTAT	TTTCGCTTTT	AATTTATTAA	360
55	CGAGAATAAT	AAATAAATAA	ATAAATAAAT	ATAAACAAAA	ATAAAAATAT	AAGAAAAGTG	420
56	TACGTGACAA	GAGCTCGAAA	AGAAGTTGCA	ACAAATAGCA	AAAATAATTC	GTGCGTGCGA	480
57	AAAAGTGCTG	CGAAGTTTTA	TGGCCCATGC	AAAAAGTGCT	AAATTTGTAA	ATGGCATGGA	540
58	AAGTGCAAAG	CTCTGATTAA	AAAACCCGCG	AAGATTGGAG	TGCGAGGTGC	CGCCCAATAA	600
59	CGCAACCAAC	TACTGCCACA	AGGAAATTAT	TAAGACCAAT	CAACGACCAA	AAAAATAAAA	660
60	AATAAAACAA	AAGCAAGCAG	AAATTTGGTG	CTAGTTCTGT	TTAGTCGACA	GCCATCCACG	720
61	TTGGATCCCC	ATCGCAAATA	ATGTCATCAA	AATGTGCTTT	CAACATTGTA	TTCGTATCGA	780
62	TCATTTTCAT	CATCATCGTA	AATGGTTACG	CAAAAGATAT	TTCTGGAGTT	AAAAGAGGTC	840
63	ATGAACGACT	TAACGAATAC	ATATCCCACT	ATGAAACACT	CAACTATGAT	CACGAGCACA	900
64	TCCGAGCTAG	TCACAATAGA	GCGCGACGAT	CAGTGACCAA	AGATCAATAT	GTACATTTAA	960
65	AGTTTGCATC	ACATGGAAGA	GACTTCCATC	TTAGATTAAA	ACGTGATTTA	AATACATTTA	1020
66	GCAATAAGTT	AGACTTTTAT	GATAGCAAAG	GTCCCATTTG	TGTCTCCACG	GATCATATCT	1080
67	ATGAGGGCGA	AGTGATAGGG	GATCGTAATA	GTTATGTATT	TGGTTCCATA	CACAATGGGG	1140
68	TATTCGAGGG	TAAAATTATA	ACGGAACGTG	ATGCCTATTA	TGTTGAACAT	GCCAAACATT	1200
69	ATTTTCCAC	AAATCGCACG	GCGACAACAA	CACCACCATC	GACTTCGACG	ACATCCTCAG	1260
70	CAACAACAGT	CACAAAAAGC	ACACAACCAA	CACGGCCTTT	GGCCAAAAGC	AACACCAGTA	1320
71	CTACTGCCGT	TAATAGTAAG	ACAGAAAAC	TTATAAAGAA	AATTGCTGAA	TCCACAACGA	1380
72	CGAGCCAGCA	GCTTCCAGAA	TATACCGAAT	CGTCGTCGTC	GTCGTCGACA	ACAACATTCC	1440
73	CACCCACAAC	AGAGTATTTT	GAGGACGAAA	AGGAGCGTAA	TGCCGAGGAC	GAAGTTGATT	1500
74	TTCACCTCAT	TATCTACAAG	GAGTCACATG	TCGAGGACGC	CTACGAAAAT	GTGCGCGAAG	1560
75	GTCACGTGGC	CGGCTGTGGC	ATCACGGATG	AGGTCTCTCA	GTGGATGGAG	AACATACAAA	1620
76	ATTCAGCCGT	CGAAGAGTTG	CCGGAGCCCA	TGTCAAAGGA	CTATCAAAAG	CTCCACCGGA	1680
77	AGCAGCTGCA	CAAAAAGTCC	GCCCCACAGC	AACAACAGCA	GCCCCATCCG	CCGAAGAAGT	1740
78	ACATCAGCGG	GGATGAGGAC	TTCAAGTATC	CCCACCAGAA	GTACACGAAG	GAAGCTAACT	1800
79	TCGCCGAGGG	TGCATTCTAC	GATCCATCGA	CCGGACGTCG	CCTGGGCTCA	TCCGCCAACG	1860
80	TGGCCGACTG	GCATCAGCTC	GTCCACGAGC	GCGTCCGCCG	CGCCACCGAC	AATGGTGCTG	1920
81	GGGATAGGGG	CTCATCCGGT	GGATCTGGAC	GCGGTCGCGA	GGACAACAAG	AATACCTGCT	1980
82	CGCTCTACAT	TCAAACGGAT	CCATTGATAT	GGCGCCACAT	ACGCGAAGGC	ATTGCTGACC	2040
83	ACGATCGTGG	ACGCAAGTAC	GAGGTGGATG	AGAAAACGCG	CGAGGAAATC	ACATCGTTGA	2100
84	TTGCACATCA	CGTGACGGCC	GTTAATTACA	TTTACCGCAA	CACAAAGTTC	GACGGACGCA	2160
85	CCGAGCATCG	CAACATACGC	TTTGAGGTGC	AACGCATTAA	GATCGATGAC	GATTGCGCCT	2220
86	GTGCAATTTC	CTACAATGGT	CCACACAATG	CCTTTTGCAA	TGAACACATG	GATGTCTCGA	2280
87	ACTTTTTGAA	TCTGCATTCC	CTAGAAGATC	ACTCGGACTT	TTGTTTGGCT	TACGTGTTCA	2340
88	CCTACAGAGA	TTTCACTGGC	GGCACTTTGG	GTCTGGCCTG	GGTGGCCAGT	GCGTCGGGAG	2400
89	CCTCTGGTGG	AATTGCGGAG	AAGTACAAGA	CGTACACGGA	AACGGTGGGT	GGACAGTACC	2460
90	AGAGCACCAA	GCGATCACTC	AACACGGGCA	TCATCACCTT	TGTCAACTAC	AACAGTCGGG	2520
91	TGCCGCCGAA	AGTGTGCGAG	CTTACGTTGG	CACACGAGAT	TGGCCACAAC	TTTGGATCAC	2580
92	CTCACGATTA	CCCTCAGGAA	TGTCGTCCTG	GTGGCCTAAA	TGGCAATTAC	ATTATGTTCT	2640
93	CCAGTGCCAC	CTCCGGTGAT	AGGCCAAATA	ACTCCAAGTT	CTCGCCCTGC	TCCATTCCGA	2700
94	ACATCTCCAA	TGTCCTTGAC	GTGCTGGTGG	GCAACACGAA	GCGCGACTGC	TTCAAGGCCT	2760
95	CGGAAGGTGC	CTTCTGCGGC	AACAAGATCG	TGGAGTCTGG	CGAGGAATGC	GACTGTGGCT	2820
96	TCAACGAGGA	GGAGTGCAAG	GACAAGTGCT	GCTACCCGCG	TCTGATCAGC	GAGTACGACC	2880
97	AGTCGCTGAA	CTCCAGTGCC	AAGGGATGCA	CGCGCCGCGC	CAAGACCCAG	TGCTCACCAT	2940
98	CGCAGGGTCC	GTGCTGTCTG	TCCAATCCTT	GCACCTTTGT	GCCGACGAGC	TACCACCAGA	3000
99	AGTGCAAGGA	GGAGACGGAG	TGCAGCTGGT	CGAGCACATG	CAACGGAACC	ACGGCCGAGT	3060
100	GTCCGGAGCC	ACGTATCGCG	GATGACAAGA	CCATGTGCAA	CAATGGAACA	GCGCTATGCA	3120
101	TCCGCGGTGA	ATGTAGTGGA	TCGCCATGTT	TGCTCTGGAA	TATGACAAAG	TGCTTCCTTA	3180

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102 CCTCGACCAC ACTGCCGCAC GTGAGCAAGC GCAAGTTGTG CGACTTGGCC TGCCAGGATG 3240
103 GCAATGACAC CTCCACCTGC CGCAGCACCA GCGAGTTTGC CGATAAATAT AATATTCAAA 3300
104 AGGGTGGTAT TAGTCTGCAG CCCGGTTTCG CATGCGATAA TTTCCAGGGC TACTGCGATG 3360
105 TGTTCCCTTAA GTGTCTGAGC GTGGATGCCG ATGGTCCGCT TCTTCGGCTG AAGAATTTGT 3420
106 TGCTCAACCG GAAGACCCTG CAAACGGTGG CCGAGTGGAT CGTCGACAAAT TGGTACCTAG 3480
107 TGGTTCTGAT GGGAGTGGCC TTTATTGTGG TCATGGGTTT GTTCATCAAA TGTTGTGCCG 3540
108 TGCACACGCC CAGTTCCAAT CCGAAGAAGC GACGAGCTCG TCGAATCAGC GAAACTCTAA 3600
109 GAGCACCCAT GAACACGTTG CGTAGAATGC AACGTCATCC CAATCAGCGA GGAGCAGGTC 3660
110 CTCGAAGCAT CCCACCGCCG GCACATGAGG CGCAGCATT TACACGCGGC GGAGATGGTC 3720
111 GCGGCGGCGG CGGTGGAGGC GGAGGTCGCC ACGGTGGCTC TAGGTCACAC CATCAACAGC 3780
112 ATCCGCACGA TTGGGATCGT CATCAGGGTG GCCACTCAAT CGTCCCATTG CCCACCGGCG 3840
113 GCAGCCATT CAGTCGCAAC TCGGCGGCGA ATCAAGCGAG AAGAAGCGAT GGACGAGGTC 3900
114 CACGATCCAC CAGCAGTGGG CGGCCGCGAG CTATAGCCAG CGGAAGCGGT GCCGCGAGCG 3960
115 GAGCAGCGCG ATCTCATGGC GGGTACGGAG CCGAACAGGC GATACCGGGT TCCATTGGTG 4020
116 GTGGTGTCCA GCGCGCCATT AGCAGCGGCG GTGTGGTGGC TCGGGCCCAG CTGCCGCTGC 4080
117 CATTGCCGCC GCCAATGGA CAGCAGCAAA TGCAACAGCA ACAACAATG CAACTACAGC 4140
118 AACC GGCAAT TTCGCCGAG CAGCAGCGCG AGCAAGCGTT CTACACGCCG AAAGAACTAC 4200
119 CACCACGCAA TAAGTCCCGA TCATCACGTA CCAACAACAC CTCCAACACC ACAACCACCA 4260
120 CCAACTCATC CACAGCGGCA GCCGGCAGTG GGTCGGTCTC GGGACCGGGC TCGGGGGCGG 4320
121 GCAGTAGTAG TAAGAGCAAG AGCGGTAAAA GTGCCAAAGC CAAAGACTCA AAGTCGCAAA 4380
122 AATCGCAGCA GGCCAACAAC AGTCGAGCA GCAGCAAGGA GAAGGGCGTC AAGCCAGTGC 4440
123 GCCGAAATAT CGTTTATTAG GAGCGGAACC ATCACATTGC CATAACAAC ACTGAACGAA 4500
124 ATATAGCCCC GAACCCAAA TATCAAATGC AACCACATAT AGAATCGCCC GCTGCTAGTC 4560
125 ATCGAACTAC ATGTATGAGT TGTTGCTTCC CATCCACCGA CAAACACAAA CAGAAAAGAA 4620
126 ATTATAATGA TATTTTATTT AATCGATGCA ATTGGCGTCG CGCCGCCTCC GCTACAAGTA 4680
127 AGCTTTAGTC GGCCGACATC GTTGCACGAG CAACAGCAGC AGCAACATCA TCTGCAGCAG 4740
128 CAGCAGCAGC ATCAGCAGCA ACTGGAGCCG CAGCAGCAAC ACGCCTATGC CGATGCTTAT 4800
129 GCGGCCTTGG GCGGGGGCCA GTATGAGTCC ACCACGCGGG CGCCCAACAA CAGCAAGGTT 4860
130 TGACAGCCAA AAGTAGCAAT GGAGCGCCAC AAAAGGCCAA AGGCTAAGCG ACTCAAGCAG 4920
131 CAGAAGGAGC CGCATACACA GCAAACAACA ACACAGCAAC AAAAGCAAAA ACAACATAAA 4980
132 TCAAATGAAC TCAAATTTAA TGTAATGTA ATTTTATATG TAATTATTTT TATTTAAACA 5040
133 GTGTTTGTAT GCCACAAGGG AAAACAGCCA GCAACAAAAA GAAAAATACA AAAATAACAC 5100
134 AAAAAAGGAG ACAAATTTTC TAATACAGAA AAAGCTGAAA GTGAATGATA TTTTGTATTA 5160
135 ACTAAATTAA AATGAAAATA CGAATGCAAA TTATGAATAA TAAAAGTAAT TAAAAACGAC 5220
136 AACATGCATA ATACATATAA AGTTGCAAGT TGCATATATA TACATTTGTA TGTATATATT 5280
137 TATTATGGAT ACACAATTAT TAAATAGCAG CAGCCACAAC AAACAAGTAA TATACATGAA 5340
138 GAAAAACTAA GGTTTAATTG TATGAGAAAG CATTCTATAT GTCGGTGAGA TTTCTAAGCG 5400
139 CTAGGCCGAA ATACAAAATT AATTACACAC TTGAATAACA AAATGTGTTT TGTACAAAAA 5460
140 AAAAAAATG AAATAAACAA AAACAGTGCG AATTAATTAA GCGTCATTAT AAAAAAAGA 5520
141 ACGGAAACAA CAAAGCATTT AAATTGTATT TATCTGTACC GAAGCTAAAC GTTTATTTAA 5580
142 AGCCGTCAA ATTGCATTTG TAAACTAGCA AAACAAAAA AAAAAAAAC 5630
144 (2) INFORMATION FOR SEQ ID NO: 2:
145 (i) SEQUENCE CHARACTERISTICS:
146 (A) LENGTH: 1239 amino acids
147 (B) TYPE: amino acid
148 (C) STRANDEDNESS: single
149 (D) TOPOLOGY: linear
150 (ii) MOLECULE TYPE: peptide
151 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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152 Met Ser Ser Lys Cys Ala Phe Asn Ile Val Phe Val Ser Ile Ile Phe
153 1 5 10 15
154 Ile Ile Ile Val Asn Gly Tyr Ala Lys Asp Ile Ser Gly Val Lys Arg
155 20 25 30
156 Gly His Glu Arg Leu Asn Glu Tyr Ile Ser His Tyr Glu Thr Leu Asn
157 35 40 45
158 Tyr Asp His Glu His Ile Arg Ala Ser His Asn Arg Ala Arg Arg Ser
159 50 55 60
160 Val Thr Lys Asp Gln Tyr Val His Leu Lys Phe Ala Ser His Gly Arg
161 65 70 75 80
162 Asp Phe His Leu Arg Leu Lys Arg Asp Leu Asn Thr Phe Ser Asn Lys
163 85 90 95
164 Leu Asp Phe Tyr Asp Ser Lys Gly Pro Ile Asp Val Ser Thr Asp His
165 100 105 110
166 Ile Tyr Glu Gly Glu Val Ile Gly Asp Arg Asn Ser Tyr Val Phe Gly
167 115 120 125
168 Ser Ile His Asn Gly Val Phe Glu Gly Lys Ile Ile Thr Glu Arg Asp
169 130 135 140
170 Ala Tyr Tyr Val Glu His Ala Lys His Tyr Phe Pro Thr Asn Arg Thr
171 145 150 155 160
172 Ala Thr Thr Thr Pro Pro Ser Thr Ser Thr Thr Ser Ser Ala Thr Thr
173 165 170 175
174 Val Thr Lys Ser Thr Gln Pro Thr Arg Pro Leu Ala Lys Ser Asn Thr
175 180 185 190
176 Ser Thr Thr Ala Val Asn Ser Lys Thr Glu Asn Phe Ile Lys Lys Ile
177 195 200 205
178 Ala Glu Ser Thr Thr Thr Ser Gln Gln Leu Pro Glu Tyr Thr Glu Ser
179 210 215 220
180 Ser Ser Ser Ser Ser Thr Thr Phe Pro Pro Thr Thr Glu Tyr Phe
181 225 230 235 240
182 Glu Asp Glu Lys Glu Arg Asn Ala Glu Asp Glu Leu Asp Phe His Ser
183 245 250 255
184 Ile Ile Tyr Lys Glu Ser His Val Glu Asp Ala Tyr Glu Asn Val Arg
185 260 265 270
186 Glu Gly His Val Ala Gly Cys Gly Ile Thr Asp Glu Val Ser Gln Trp
187 275 280 285
188 Met Glu Asn Ile Gln Asn Ser Ala Val Glu Glu Leu Pro Glu Pro Met
189 290 295 300
190 Ser Lys Asp Tyr Gln Lys Leu His Arg Lys Gln Leu His Lys Lys Ser
191 305 310 315 320
192 Ala Pro Gln Gln Gln Gln Pro His Pro Pro Lys Lys Tyr Ile Ser
193 325 330 335
194 Gly Asp Glu Asp Phe Lys Tyr Pro His Gln Lys Tyr Thr Lys Glu Ala
195 340 345 350
196 Asn Phe Ala Glu Gly Ala Phe Tyr Asp Pro Ser Thr Gly Arg Arg Leu
197 355 360 365
198 Gly Ser Ser Ala Asn Val Ala Asp Trp His Gln Leu Val His Glu Arg
199 370 375 380
200 Val Arg Arg Ala Thr Asp Asn Gly Ala Gly Asp Arg Gly Ser Ser Gly

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201	385				390					395				400
202	Gly	Ser	Gly	Arg	Gly	Arg	Glu	Asp	Asn	Lys	Asn	Thr	Cys	Ser
203					405					410				415
204	Ile	Gln	Thr	Asp	Pro	Leu	Ile	Trp	Arg	His	Ile	Arg	Glu	Gly
205				420					425					430
206	Asp	His	Asp	Arg	Gly	Arg	Lys	Tyr	Glu	Val	Asp	Glu	Lys	Thr
207				435				440					445	
208	Glu	Ile	Thr	Ser	Leu	Ile	Ala	His	His	Val	Thr	Ala	Val	Asn
209				450			455					460		
210	Tyr	Arg	Asn	Thr	Lys	Phe	Asp	Gly	Arg	Thr	Glu	His	Arg	Asn
211							470					475		480
212	Phe	Glu	Val	Gln	Arg	Ile	Lys	Ile	Asp	Asp	Asp	Ser	Ala	Cys
213					485				490					495
214	Ser	Tyr	Asn	Gly	Pro	His	Asn	Ala	Phe	Cys	Asn	Glu	His	Met
215				500					505					510
216	Ser	Asn	Phe	Leu	Asn	Leu	His	Ser	Leu	Glu	Asp	His	Ser	Asp
217			515					520					525	
218	Leu	Ala	Tyr	Val	Phe	Thr	Tyr	Arg	Asp	Phe	Thr	Gly	Gly	Thr
219			530				535					540		
220	Leu	Ala	Trp	Val	Ala	Ser	Ala	Ser	Gly	Ala	Ser	Gly	Gly	Ile
221						550				555				560
222	Lys	Tyr	Lys	Thr	Tyr	Thr	Glu	Thr	Val	Gly	Gly	Gln	Tyr	Gln
223					565				570					575
224	Lys	Arg	Ser	Leu	Asn	Thr	Gly	Ile	Ile	Thr	Phe	Val	Asn	Tyr
225				580					585					590
226	Arg	Val	Pro	Pro	Lys	Val	Ser	Gln	Leu	Thr	Leu	Ala	His	Glu
227			595				600						605	
228	His	Asn	Phe	Gly	Ser	Pro	His	Asp	Tyr	Pro	Gln	Glu	Cys	Arg
229			610				615					620		
230	Gly	Leu	Asn	Gly	Asn	Tyr	Ile	Met	Phe	Ala	Ser	Ala	Thr	Ser
231					630						635			640
232	Arg	Pro	Asn	Asn	Ser	Lys	Phe	Ser	Pro	Cys	Ser	Ile	Arg	Asn
233					645					650				655
234	Asn	Val	Leu	Asp	Val	Leu	Val	Gly	Asn	Thr	Lys	Arg	Asp	Cys
235				660				665						670
236	Ala	Ser	Glu	Gly	Ala	Phe	Cys	Gly	Asn	Lys	Ile	Val	Glu	Ser
237			675					680					685	
238	Glu	Cys	Asp	Cys	Gly	Phe	Asn	Glu	Glu	Glu	Cys	Lys	Asp	Lys
239			690				695					700		
240	Tyr	Pro	Arg	Leu	Ile	Ser	Glu	Tyr	Asp	Gln	Ser	Leu	Asn	Ser
241						710				715				720
242	Lys	Gly	Cys	Thr	Arg	Arg	Ala	Lys	Thr	Gln	Cys	Ser	Pro	Ser
243					725					730				735
244	Pro	Cys	Cys	Leu	Ser	Asn	Ser	Cys	Thr	Phe	Val	Pro	Thr	Ser
245				740					745					750
246	Gln	Lys	Cys	Lys	Glu	Glu	Thr	Glu	Cys	Ser	Trp	Ser	Ser	Thr
247			755					760					765	
248	Gly	Thr	Thr	Ala	Glu	Cys	Pro	Glu	Pro	Arg	His	Arg	Asp	Asp
249			770				775						780	

## VERIFICATION SUMMARY

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L:25 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:26 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]